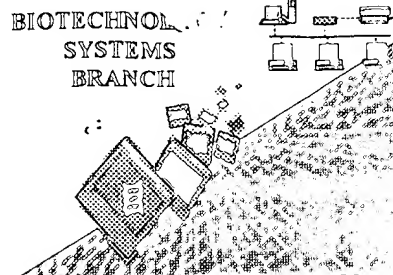# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/842,930_

Source: _OIPE_

Date Processed by STIC: _5/11/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid
Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>**
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or **Xaa** represents.

11 _____ Use of "Artificial"
(NEW RULES)
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature
(NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

OIPE

```
RAW SEQUENCE LISTING                    DATE: 05/11/2001
PATENT APPLICATION:  US/09/842,930      TIME: 15:27:41
```

Does Not Comply
Corrected Diskette Needed
TR 1-5

```
Input Set : A:\SEQUENCES.txt
Output Set: N:\CRF3\05112001\I842930.raw
```

```
        4 <110> APPLICANT: Weigel et al.
W-->    5 <120> TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
W-->    6 <130> FILE REFERENCE: 5820.603
W-->    7 <140> CURRENT APPLICATION NUMBER: Not Yet Assigned
C-->    8 <141> CURRENT FILING DATE: 2001-04-25
E-->    9 <160> NUMBER OF SEQ ID: 57
       10 <170> SOFTWARE: WordPerfect 8.0 *Software*
```


ERRORED SEQUENCES

```
W-->   11 <210> SEQ ID NO: 1
       12 <211> LENGTH: 4706
       13 <212> TYPE: DNA
       14 <213> ORGANISM: Rattus Norvegicus
W-->   15 <220> FEATURE:
E-->   16 <400> SEQUENCE: 0
C-->   19
```

```
       21                              tctttaccaa gtctactcac ccgtctggag ca

       23                              tacattattc attacaacct ggcaagtgca at

       25                              gtgccaaaca atgaagccat cgaaaactat at

       27                              gaagatattc tacggtacca tgtggtcctg gg

       29                              aacggcatgc accgagagac catgctgggg tt

       31                              aatgaccagc tgtatgtaaa tgaagctcca at

       33                              ggagtgatcc atggtctgga gaaagttctg ga

       35                              gacaccatta ttgtgagagg ggagtgtgga aa

       37                              gagacaaaac cacttagaga gacgaggaaa tg

       39                              agatccgtat tcatcgggtg ccagccacag tg

       41                              tggctggctt ctttggccca caatgccaag cc

       43                              ctgggaacgg cttctgtctg ggacggtgtg aa

       45                              ggcttcaatg ggacagcctg tgaaacctgc ac

       47                              caagcatgct cttgtgtcca tgggagatgt ag

       49                              gactgtgacg tcggctggcg aggagtgaag tg

       51                              aacgggacct gtcacaccag tgccaactgc ct

       53                              aaatgtgcgg caggattccg agggaatgga ac

       55                              accagcaatg gaggatgttc tacaaaggcc ga

                                       gtgtgtgtgt gcaaggcagg ctataccggc ga
```

see p. 2
for exploration

~~SEQUENCE LISTING~~ *delete*

```
<110> Weigel et al.
<120> Identification of Hyaluronan Receptor for Endocytosis
<130> 5820.603
<140> Not Yet Assigned
<141> Herewith
<160> 57
<170> WordPerfect 8.0 *Software*
<210> 1
<211> 4706
<212> DNA
<213> Rattus Norvegicus
<220>
<223> <400> HARE CDNA
```

This line contains features ↓

<223>

(400) 1 ← This mandatory numeric identifier and response appear before each sequence

```
GTCTACTCAC CCGTCTGGAG CAGATGCCCG ACTATTCCAT TTTCCGAGGT      60    TCTTTACCAA

ATTACAACCT GGCAAGTGCA ATCGAGTCTG CAGATGCTTA TACTGTGTTC     120    TACATTATTC

ATGAAGCCAT CGAAAACTAT ATCAGGGAGA AGAAAGCCAC ATCTCTAAAG     180    GTGCCAAACA

TACGGTACCA TGTGGTCCTG GGGGAAAAGC TCCTGAAGAA TGACTTGCAT     240    GAAGATATTC

ACCGAGAGAC CATGCTGGGG TTCTCCTACC TCCTTGCCTT CTTTCTCCGC     300    AACGGCATGC
```

Per 1.822 of Sequence Rules, group all non-coding bases into 10's on same line, with cumulative base total figure at right margin of each line. 60 bases per line — all bases must be in lower-case letters when in new Sequence Rules format.

Please follow this format for all nucleic acid sequences throughout Sequence Listing.

RAW SEQUENCE LISTING   DATE: 05/11/2001
PATENT APPLICATION: US/09/842,930   TIME: 15:27:41

Input Set : A:\SEQUENCES.txt
Output Set: N:\CRF3\05112001\I842930.raw

```
W--> 195 <110> APPLICANT: Weigel et al.
W--> 195 <110> APPLICANT: Weigel et al.
W--> 196 <120> TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
W--> 196 <120> TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
W--> 196 <120> TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
W--> 197 <130> FILE REFERENCE: 5820.603
W--> 197 <130> FILE REFERENCE: 5820.603
W--> 197 <130> FILE REFERENCE: 5820.603
W--> 198 <140> CURRENT APPLICATION NUMBER: Not Yet Assigned
     199 <141> CURRENT FILING DATE: Herewith
W--> 200 <160> NUMBER OF SEQ ID: 57
W--> 200 <160> NUMBER OF SEQ ID NOS: 57
W--> 200 <160> NUMBER OF SEQ ID NOS: 57
W--> 201 <170> SOFTWARE: WordPerfect 8.0 *Software*
W--> 202 <210> SEQ ID NO: 2
     203 <211> LENGTH: 1431
     204 <212> TYPE: PRT
     205 <213> ORGANISM: Rattus norvegicus
W--> 206 <220> FEATURE:
E--> 207 <400> SEQUENCE: 0
E--> 211 Ser Leu Pro Ser Leu Leu Thr Arg Leu Glu Gln Met Pro Asp Tyr Ser Iso Phe Arg
     212 1               5                   10              15
E--> 214 Gly Tyr Iso Iso His Tyr Asn Leu Ala Ser Ala Iso Glu Ser Ala Asp Ala Tyr Thr
     215 20                  25                  30                  35
E--> 217 Val Phe Val Pro Asn Asn Glu Ala Iso Glu Asn Tyr Iso Arg Glu Lys Lys Ala
     218    40                  45                  50                  55
E--> 220 Thr Ser Leu Lys Glu Asp Iso Leu Arg Tyr His Val Val Leu Gly
     221              60              65              70
     223 Glu Lys Leu Leu Lys Asn Asp Leu His Asn Gly Met His Arg Glu Thr Met
     224          75              80              85
     227 Leu Gly Phe Ser Tyr Leu Leu Ala Phe Phe Leu Arg Asn Asp Gln Leu Tyr Val Asn
     228    90              95              100             105
E--> 230 Glu Ala Pro Iso Asn Tyr Thr Asn Val Ala Thr Asp Lys Gly Val Iso His Gly Leu
     231          110             115             120             125
E--> 233 Glu Lys Val Leu Glu Iso Gln Lys Asn Arg Cys Asp Asn Asn Asp Thr Iso Iso Val
     234          130             135             140             145
     236 Arg Gly Glu Cys Gly Lys Cys Ser Gln Gln Ala Pro Cys Pro Leu Glu Thr Lys Pro
     237          150             155             160
E--> 239 Leu Arg Glu Thr Arg Lys Cys Iso Tyr Ser Iso Tyr Phe Met Gly Lys Arg Ser Val
     240 165             170             175             180
E--> 243 Phe Iso Gly Cys Gln Pro Gln Cys Val Arg Thr Iso Iso Thr Arg Ala Cys Trp Leu
     244      185             190             195             200
     246 Ala Ser Leu Ala His Asn Ala Lys Pro Ala Pro Gly Glu Val Lys Met Cys Ala Leu
     247          205             210             215             220
     249 Gly Thr Ala Ser Val Trp Asp Gly Val Asn Gly Thr Gly Thr Cys Gln Cys Gly Leu
     250          225             230             235             240
E--> 252 Gly Phe Asn Gly Thr Ala Cys Glu Thr Cys Thr Glu Gly Lys Tyr Gly Iso His Cys
     253          245             250             255
     255 Asp Gln Ala Cys Ser Cys Val His Gly Arg Cys Ser Gln Gly Pro Leu Gly Asp Gly
```

```
<110> Weigel et al.
<120> Identification of Hyaluronan Receptor for Endocytosis
<130> 5820.603
<140> Not Yet Assigned
<141> Herewith
<160> 57
<170> WordPerfect 8.0 *Software*
<210> 2
<211> 1431
<212> PRT
<213> Rattus norvegicus
<220>
<223> <400> HARE protein
```

This section ONLY appears once, at beginning of Sequence Listing.

```
<400> 2
```

Per 1.822 of Sequence Rules, a MAXIMUM of 16 amino acids per line allowed.

```
Ser Leu Pro Ser Leu Leu Thr Arg Leu Glu Gln Met Pro Asp Tyr Ser Iso Phe Arg
1           5                   10              15
```
invalid - use Ile for Isoleucine

```
Gly Tyr Iso Iso His Tyr Asn Leu Ala Ser Ala Iso Glu Ser Ala Asp Ala Tyr Thr
20              25                  30              35
```

Please consult WIPO Standard ST.25, appendix 2, Tables 1-4, for correct nucleotide and amino acid format.

The above is a sample of global error. Please edit all amino acid sequences.

delete section

```
<110> Weigel et al.
<120> Identification of Hyaluronan Receptor for Endocytosis
<130> 5820.603
<140> Not Yet Assigned
<141> Herewith
<160> 5
<170> WordPerfect 8.0 *Software*
<210> 3
<211> 20
<212> DNA
<213> Rattus norvegicus
<220>
<223> <400> Primer 208F
       <400> 3
```

→ *invalid for use in the sequence*

TNTTYGCICC   20   CGNTTYACNG

*Move these onto **same** line, with cumulative
base total figure at right margin of the line*

*1) Use lower-case letters for **all** bases*

*2) See item 10 on Error Summary Sheet regarding
use of **n's** in a sequence, and **Xaa's** in an
amino acid sequence*

(Appendix 2, WIPO Standard ST.25)

*3) See Tables 1 and 2 regarding use of modified
or unusual nucleotides*

*4) See sample Sequence Listing (attached) for valid
format.*

```
<110>        Smith, John;  Smithgene Inc.

<120>        Example of a Sequence Listing

<130>        01-00001

<140>        PCT/EP98/00001
<141>        1998-12-31

<150>        US 08/999,999
<151>        1997-10-15

<160>        4

<170>        PatentIn version 2.0

<210>        1
<211>        389
<212>        DNA
<213>        Paramecium sp.

<220>
<221>        CDS
<222>        (279)...(389)

<300>
<301>        Doe, Richard
<302>        Isolation and Characterization of a Gene Encoding a
             Protease from Paramecium sp.
<303>        Journal of Genes
<304>        1
<305>        4
<306>        1-7
<307>        1988-06-31
<308>        123456
<309>        1988-06-31

<400>        1
agctgtagtc  attcctgtgt  cctcttctct  ctgggcttct  caccctgcta  atcagatctc       60

agggagagtg  tcttgaccct  cctctgcctt  tgcagcttca  caggcaggca  ggcaggcagc      120

tgatgtggca  attgctggca  gtgccacagg  cttttcagcc  aggcttaggg  tgggttccgc      180

cgcggcgcgg  cggcccctct  cgcgctcctc  tcgcgcctct  ctctcgctct  cctctcgctc      240
```

Appendix 3, page 2

```
ggacctgatt   aggtgagcag   gaggaggggg   cagttagc        atg  gtt  tca  atg  ttc  agc   296
                                                        Met  Val  Ser  Met  Phe  Ser
                                                         1                    5

ttg  tct  ttc  aaa  tgg  cct  gga  ttt  tgt  ttg  ttt  gtt  tgt  ttg  ttc  caa   344
Leu  Ser  Phe  Lys  Trp  Pro  Gly  Phe  Cys  Leu  Phe  Val  Cys  Leu  Phe  Gln
              10                  15                      20

tgt  ccc  aaa  gtc  ctc  ccc  tgt  cac  tca  tca  ctg  cag  ccg  aat  ctt ·   389
Cys  Pro  Lys  Val  Leu  Pro  Cys  His  Ser  Ser  Leu  Gln  Pro  Asn  Leu ·
              25                  30                      35
```

```
<210>        2
<211>        37
<212>        PRT
<213>        Paramecium sp.


<400>        2
Met  Val  Ser  Met  Phe  Ser  Leu  Ser  Phe  Lys  Trp  Pro  Gly  Phe  Cys  Leu
 1                  5                  10                      15

Phe  Val  Cys  Leu  Phe  Gln  Cys  Pro  Lys  Val  Leu  Pro  Cys  His  Ser  Ser
              20                  25                      30

Leu  Gln  Pro  Asn  Leu
              35


<210>        3
<211>        11
<212>        PRT
<213>        Artificial Sequence


<220>
<223>        Designed peptide based on size and polarity to act as a
             linker between the alpha and beta chains of Protein XYZ.

<400>        3
Met  Val  Asn  Leu  Glu  Pro  Met  His  Thr  Glu  Ile
 1                  5                  10


<210>        4
<400>        4
000
```

[Annex VIII follows]

identifiers and their accompanying information as shown in the following
table. The numeric identifier shall be used only in the "Sequence
Listing." The order and presentation of the items of information in the
"Sequence Listing" shall conform to the arrangement given below. Each
item of information shall begin on a new line and shall begin with the
numeric identifier enclosed in angle brackets as shown. The submission
of those items of information designated with an "M" is mandatory. The
submission of those items of information designated with an "O" is
optional. Numeric identifiers <110> through <170> shall only be set
forth at the beginning of the "Sequence Listing." The following table
illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence mole- cule is DNA, RNA, or PRT (protein). If a nucleotide sequence con- tains both DNA and RNA frag- ments, the type shall be "DNA." In ad- dition, the combined DNA/ RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artifi- cial Sequence. In addition, the "Unknown" or "Artificial Se- quence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of bio- logical signi- ficance in the sequence.	M, under the following condi- tions: if "n," "Xaa," or a mod- ified or unusual L-amino acid or modified base was used in a se- quence; if ORGAN- ISM is "Artifi- cial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, pre- ferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the fol- lowing conditions: if "n," "Xaa," or a modified or un- usual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the fol- lowing conditions: if "n," "Xaa," or a modified or un- usual L-amino acid or modified

		in feature	base was used in a sequence
<223>	Other Infor-mation	Other relevant information; four lines maximum	M, under the fol-lowing conditions: if "n," "Xaa," or a modified or un-usual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is com-bined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	O
<301>	Authors	Preferably max of ten named authors of publi-cation; specify one name per line; preferable format: Surname, Other Names and/or Initials	O
<302>	Title		O
<303>	Journal		O
<304>	Volume		O
<305>	Issue		O
<306>	Pages		O
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	O
<308>	Database Accession Number	Accession number assigned by data-base including database name	O
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	O
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	O

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	O
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	M

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by   1.821(e) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;

Input Set : **A:\SEQUENCES.txt**
Output Set: **N:\CRF3\05112001\I842930.raw**

L:5 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:283 W: Missing Blank Line separator, <140> field identifier
L:7 M:270 C: Current Application Number differs, Replaced Current Application Number
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:11 M:283 W: Missing Blank Line separator, <210> field identifier
L:15 M:283 W: Missing Blank Line separator, <220> field identifier
L:16 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:1 differs:0
L:16 M:283 W: Missing Blank Line separator, <400> field identifier
L:19 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=1
L:79 M:254 E: No. of Bases conflict, LENGTH:Input:1820 Counted:1860 SEQ:1
L:195 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:195 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:196 M:283 W: Missing Blank Line separator, <120> field identifier
L:196 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:196 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:197 M:283 W: Missing Blank Line separator, <130> field identifier
L:197 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:197 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:198 M:283 W: Missing Blank Line separator, <140> field identifier
L:198 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:198 M:270 C: Current Application Number differs, Replaced Current Application Number
L:199 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:199 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:199 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:200 M:283 W: Missing Blank Line separator, <160> field identifier
L:200 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:200 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
L:201 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:202 M:283 W: Missing Blank Line separator, <210> field identifier
L:206 M:283 W: Missing Blank Line separator, <220> field identifier
L:207 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:0
L:207 M:283 W: Missing Blank Line separator, <400> field identifier
L:211 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:214 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:217 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:220 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:230 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:233 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:239 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:243 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:252 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:258 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:267 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:270 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:273 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

Input Set : A:\SEQUENCES.txt
Output Set: N:\CRF3\05112001\I842930.raw

```
L:279 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:282 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:285 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:294 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:300 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:303 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:306 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:312 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:321 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:324 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:327 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:330 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:333 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:336 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:339 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:346 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
M:332 Repeated in SeqNo=2
L:354 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:360 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:369 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:384 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:393 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:405 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:408 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:414 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:417 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:420 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:423 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:429 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:435 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:485 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:485 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:486 M:283 W: Missing Blank Line separator, <120> field identifier
L:486 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:486 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:487 M:283 W: Missing Blank Line separator, <130> field identifier
L:487 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:487 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:488 M:283 W: Missing Blank Line separator, <140> field identifier
L:488 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:488 M:270 C: Current Application Number differs, Replaced Current Application Number
L:489 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:489 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:489 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:490 M:283 W: Missing Blank Line separator, <160> field identifier
L:490 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:490 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
L:491 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:492 M:283 W: Missing Blank Line separator, <210> field identifier
```

Input Set : A:\SEQUENCES.txt
Output Set: N:\CRF3\05112001\I842930.raw

```
L:496 M:283 W: Missing Blank Line separator, <220> field identifier
L:497 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:0
L:497 M:283 W: Missing Blank Line separator, <400> field identifier
L:500 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:0
L:500 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:0
L:500 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:0
L:500 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:500 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:500 M:112 C: (48) String data converted to lower case,
L:534 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:534 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:535 M:283 W: Missing Blank Line separator, <120> field identifier
L:535 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:535 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:536 M:283 W: Missing Blank Line separator, <130> field identifier
L:536 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:536 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:537 M:283 W: Missing Blank Line separator, <140> field identifier
L:537 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:537 M:270 C: Current Application Number differs, Replaced Current Application Number
L:538 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:538 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:538 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:539 M:283 W: Missing Blank Line separator, <160> field identifier
L:539 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:539 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
L:540 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:541 M:283 W: Missing Blank Line separator, <210> field identifier
L:545 M:283 W: Missing Blank Line separator, <220> field identifier
L:546 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:4 differs:0
L:546 M:283 W: Missing Blank Line separator, <400> field identifier
L:549 M:112 C: (48) String data converted to lower case,
L:583 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:583 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:584 M:283 W: Missing Blank Line separator, <120> field identifier
L:584 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:584 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:585 M:283 W: Missing Blank Line separator, <130> field identifier
L:585 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:585 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:586 M:283 W: Missing Blank Line separator, <140> field identifier
L:586 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:586 M:270 C: Current Application Number differs, Replaced Current Application Number
L:587 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:587 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:587 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:588 M:283 W: Missing Blank Line separator, <160> field identifier
L:588 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:588 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
```

VERIFICATION SUMMARY   DATE: 05/11/2001
PATENT APPLICATION: US/09/842,930   TIME: 15:27:43

Input Set : A:\SEQUENCES.txt
Output Set: N:\CRF3\05112001\I842930.raw

```
L:589 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:590 M:283 W: Missing Blank Line separator, <210> field identifier
L:594 M:283 W: Missing Blank Line separator, <220> field identifier
L:595 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:5 differs:0
L:595 M:283 W: Missing Blank Line separator, <400> field identifier
L:599 M:112 C: (48) String data converted to lower case,
L:632 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:632 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:633 M:283 W: Missing Blank Line separator, <120> field identifier
L:633 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:633 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:634 M:283 W: Missing Blank Line separator, <130> field identifier
L:634 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:634 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:635 M:283 W: Missing Blank Line separator, <140> field identifier
L:635 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:635 M:270 C: Current Application Number differs, Replaced Current Application Number
L:636 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:636 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:636 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:637 M:283 W: Missing Blank Line separator, <160> field identifier
L:637 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:637 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
L:638 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:639 M:283 W: Missing Blank Line separator, <210> field identifier
L:643 M:283 W: Missing Blank Line separator, <220> field identifier
L:644 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:6 differs:0
L:644 M:283 W: Missing Blank Line separator, <400> field identifier
L:647 M:112 C: (48) String data converted to lower case,
L:681 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:681 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:682 M:283 W: Missing Blank Line separator, <120> field identifier
L:682 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:682 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:683 M:283 W: Missing Blank Line separator, <130> field identifier
L:683 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:683 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:684 M:283 W: Missing Blank Line separator, <140> field identifier
L:684 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:684 M:270 C: Current Application Number differs, Replaced Current Application Number
L:685 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:685 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:685 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:686 M:283 W: Missing Blank Line separator, <160> field identifier
L:686 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:686 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
L:687 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:688 M:283 W: Missing Blank Line separator, <210> field identifier
L:692 M:283 W: Missing Blank Line separator, <220> field identifier
```

Input Set : **A:\SEQUENCES.txt**
Output Set: **N:\CRF3\05112001\I842930.raw**

```
L:693 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:7 differs:0
L:693 M:283 W: Missing Blank Line separator, <400> field identifier
L:696 M:112 C: (48) String data converted to lower case,
L:730 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:730 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:731 M:283 W: Missing Blank Line separator, <120> field identifier
L:731 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:731 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:732 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:732 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:733 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:733 M:270 C: Current Application Number differs, Replaced Current Application Number
L:734 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:734 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:734 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:735 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:735 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
L:736 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:742 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:8 differs:0
L:779 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:779 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:780 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:780 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:781 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:781 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:782 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:782 M:270 C: Current Application Number differs, Replaced Current Application Number
L:783 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:783 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:783 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:784 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:784 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
L:785 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:791 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:9 differs:0
L:828 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:828 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:829 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:829 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:831 M:270 C: Current Application Number differs, Replaced Current Application Number
L:832 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:840 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:10 differs:0
L:880 M:270 C: Current Application Number differs, Replaced Current Application Number
L:881 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:889 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:11 differs:0
L:892 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:929 M:270 C: Current Application Number differs, Replaced Current Application Number
L:930 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:938 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:12 differs:0
L:978 M:270 C: Current Application Number differs, Replaced Current Application Number
```

Input Set : A:\SEQUENCES.txt
Output Set: N:\CRF3\05112001\I842930.raw

```
L:979  M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:987  M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:13 differs:0
L:990  M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1027 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1028 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1036 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:14 differs:0
L:1039 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1076 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1077 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1085 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:15 differs:0
L:1125 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1126 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1134 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:16 differs:0
L:1137 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:0
L:1137 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:0
L:1137 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:0
L:1137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1137 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1137 M:112 C: (48) String data converted to lower case,
L:1174 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1175 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1183 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:17 differs:0
L:1186 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:0
L:1186 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:0
L:1186 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:0
L:1186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1186 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1186 M:112 C: (48) String data converted to lower case,
L:1223 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1224 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1232 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:18 differs:0
L:1235 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:0
L:1235 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:0
L:1235 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:0
L:1235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1235 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1235 M:112 C: (48) String data converted to lower case,
L:1272 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1273 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1281 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:19 differs:0
L:1285 M:112 C: (48) String data converted to lower case,
L:1321 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1322 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1330 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:20 differs:0
L:1334 M:112 C: (48) String data converted to lower case,
L:1370 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1371 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1379 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:21 differs:0
L:1383 M:112 C: (48) String data converted to lower case,
```

Input Set : **A:\SEQUENCES.txt**
Output Set: **N:\CRF3\05112001\I842930.raw**

L:1419 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1420 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1428 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:22 differs:0
L:1431 M:112 C: (48) String data converted to lower case,
L:1468 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1469 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1477 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:23 differs:0
L:1480 M:112 C: (48) String data converted to lower case,
L:1517 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1518 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1526 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:24 differs:0
L:1529 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=24
L:1614 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1615 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1623 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:25 differs:0
L:1627 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:1630 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:1838 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
M:332 Repeated in SeqNo=25
L:1860 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1861 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1869 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:26 differs:0
L:1872 M:112 C: (48) String data converted to lower case,
L:1909 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1910 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1918 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:27 differs:0
L:1958 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1959 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1967 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:28 differs:0
L:2007 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2008 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2016 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:29 differs:0
L:2019 M:112 C: (48) String data converted to lower case,
L:2056 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2057 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2065 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:30 differs:0
L:2068 M:112 C: (48) String data converted to lower case,
L:2105 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2106 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2114 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:31 differs:0
L:2117 M:112 C: (48) String data converted to lower case,
L:2154 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2155 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2163 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32 differs:0
L:2166 M:112 C: (48) String data converted to lower case,
L:2203 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2204 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2212 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:33 differs:0

```
L:2215 M:112 C: (48) String data converted to lower case,
L:2252 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2253 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2261 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:34 differs:0
L:2264 M:112 C: (48) String data converted to lower case,
L:2301 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2302 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2310 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:35 differs:0
L:2313 M:112 C: (48) String data converted to lower case,
L:2350 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2351 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2359 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:36 differs:0
L:2362 M:112 C: (48) String data converted to lower case,
L:2399 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2400 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2403 M:214 E: (33) Seq.# missing, SEQ ID NO:37
L:2408 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:38 differs:0
L:2411 M:112 C: (48) String data converted to lower case,
L:2448 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2449 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2457 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:39 differs:0
L:2460 M:112 C: (48) String data converted to lower case,
L:2497 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2498 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2506 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:40 differs:0
L:2509 M:112 C: (48) String data converted to lower case,
L:2546 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2547 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2555 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:41 differs:0
L:2595 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2596 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2604 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:42 differs:0
L:2644 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2645 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2653 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:43 differs:0
L:2693 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2694 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2702 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:44 differs:0
L:2742 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2743 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2751 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:45 differs:0
L:2791 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2792 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2800 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:46 differs:0
L:2840 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2841 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2849 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:47 differs:0
L:2889 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2890 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
```

Input Set : **A:\SEQUENCES.txt**
Output Set: **N:\CRF3\05112001\I842930.raw**

```
L:2898 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:48 differs:0
L:2938 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2939 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2947 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:49 differs:0
L:2987 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2988 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2996 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:50 differs:0
L:3036 M:270 C: Current Application Number differs, Replaced Current Application Number
L:3037 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:3045 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:51 differs:0
L:3086 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:3332 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (57) Counted (56)
```